

AMENDMENT TO THE SPECIFICATION

Please amend the specification as described below.

Please replace paragraphs [0209]-[0214] with the following paragraph.

--[0209] The nucleotide sequence of each of a plurality of GAM oligonucleotides that are described by Fig. 1 and their respective genomic sequences and genomic locations are set forth in Tables 1-3, hereby incorporated herein. Specifically, in Table 1, line 241237, GAM RNA (miRNA) as set forth in SEQ ID NO: 117937 is shown as predicted from human herpesvirus 5.

GAM	GAM NAME	GAM RNA SEQUENCE	GAM ORGANISM	GAM
SEQ-ID				POS
=====	=====	=====	=====	=====
117937	GAM501831	AGTGACGGTGAGATCCAGGCTG	Human herpesvirus 5	A

In Table 2, lines 4474648-4474741, describes GAM PRECURSOR RNA (hairpin) as set forth in SEQ ID NO: 4204050 and as it relates to Figures 1-8.

GAM NAME	GAM	PRECUR	PRECURSOR	GAM DESCRIPTION
	ORGANISM	SEQ-ID	SEQUENCE	
=====	=====	=====	=====	=====
GAM501831	Human herp	420405	GACAGCCTCC	Fig. 1 further provides a conceptual description of another novel,
	esvirus 5	0	GGATCACATG	bioinformatically-detected viral oligonucleotide of the present invention,
			GTTACTCAGC	encoded by the Human herpesvirus 5 genome, referred to here as the Genomic
			GTCTGCCAGC	Address Messenger 501831 (GAM501831) oligonucleotide, which modulates
			CTAAGTGACG	expression of respective target genes whose function and utility are known
			GTGAGATCCA	in the art.
			GGCTGTC	GAM501831 is a novel, bioinformatically detectable, regulatory,
				non-protein-coding, miRNA-like oligonucleotide. The method by which
				GAM501831 is detected is described with additional reference to Figs. 1-8.
				The GAM501831 precursor, herein designated GAM PRECURSOR, is encoded by the
				Human herpesvirus 5 genome , which is a DNA virus. GAM501831 target gene,
				herein designated GAM TARGET GENE, is a target gene encoded by a target
				organism specified in Tables 6-7.

The GAM501831 precursor, herein designated GAM PRECURSOR, encodes a GAM501831 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA oligonucleotides, the GAM501831 precursor RNA does not encode a protein.

GAM501831 precursor RNA folds onto itself, forming GAM501831 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional "hairpin" structure. As is well-known in the art, this "hairpin structure" is typical of RNA encoded by known miRNA precursor oligonucleotides and is due to the full or partial complementarity of the nucleotide sequence of the first half of an miRNA precursor to the nucleotide sequence of the second half thereof.

A nucleotide sequence that is identical or highly similar to the nucleotide sequence of the GAM501831 precursor RNA is designated SEQ ID NO:4204050, and is provided hereinbelow with reference to the sequence listing section.

The nucleotide sequence designated SEQ ID NO:4204050 is located from position 164118 to position 164184 relative to the source sequence NC_001347 (GenBank, NCBI), on the "+" strand on the genome of Human herpesvirus 5... A schematic representation of a predicted secondary folding of GAM501831 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA is set forth in Table 4 incorporated herein.

An enzyme complex composed of Dicer RNaseIII together with other necessary proteins, designated DICER COMPLEX, cuts the GAM501831 folded precursor RNA yielding a single-stranded, ~22 nt-long RNA segment designated GAM501831 RNA, herein designated GAM RNA. Table 5 provides two possible nucleotide sequences of GAM501831 RNA: a nucleotide sequence that is highly likely to be identical or extremely similar to the nucleotide sequence of GAM501831 RNA and an alternative nucleotide sequence thereof, hereby incorporated herein.

GAM501831 target gene, herein designated GAM TARGET GENE, encodes a

corresponding messenger RNA, designated GAM501831 target RNA, herein designated GAM TARGET RNA. As is typical of mRNA of a protein-coding gene, GAM501831 target RNA comprises three regions: a 5' untranslated region, a protein-coding region and a 3' untranslated region, designated 5'UTR, PROTEIN-CODING and 3'UTR, respectively.

GAM501831 RNA, herein designated GAM RNA binds complementarily to one or more target binding sites located in the untranslated regions of GAM501831 target RNA. This complementary binding is due to the partial or full complementarity between the nucleotide sequence of GAM501831 RNA and the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 1 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III, respectively. It is appreciated that the number of target binding sites shown in Fig. 1 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig. 1 shows target binding sites only in the 3'UTR region, these target binding sites may instead be located in the 5'UTR region or in both the 3'UTR and 5'UTR regions.

The complementary binding of GAM501831 RNA, herein designated GAM RNA to target binding sites on GAM501831 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits the translation of GAM501831 target RNA into respective GAM501831 target protein, herein designated GAM TARGET PROTEIN, shown surrounded by a broken line.

It is appreciated that the GAM501831 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM501831 target genes. The mRNA of each one of this plurality of GAM501831 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM501831 RNA, herein designated GAM RNA and which when bound by GAM501831 RNA causes inhibition of translation of the

GAM501831 target mRNA into a corresponding GAM501831 target protein.

The mechanism of the translational inhibition that is exerted by GAM501831

RNA, herein designated GAM RNA on one or more GAM501831 target genes, herein

collectively designated GAM TARGET GENE, may be similar or identical to the

known mechanism of translational inhibition exerted by known miRNA

oligonucleotides.

The nucleotide sequence of GAM501831 precursor RNA, herein designated GAM

PRECURSOR RNA, its respective genomic source and genomic location and a

schematic representation of a predicted secondary folding of GAM501831

folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA are set

forth in Tables 3-4, hereby incorporated herein.

The nucleotide sequences of a "diced" GAM501831 RNA, herein designated GAM

RNA from GAM501831 folded precursor RNA are set forth in Table 5, hereby

incorporated herein. The nucleotide sequences of target binding sites, such

as BINDING SITE I, BINDING SITE II and BINDING SITE III of Fig. 1, found on

GAM501831 target RNA, herein designated GAM TARGET RNA, and a schematic

representation of the complementarity of each of these target binding sites

to GAM501831 RNA, herein designated GAM RNA are set forth in Tables 6-7,

hereby incorporated herein.

It is appreciated that the specific functions and accordingly the utilities

of GAM501831 RNA are correlated with and may be deduced from the identity of

the GAM501831 target gene inhibited thereby, and whose functions are set

forth in Table 8, hereby incorporated herein.

Table 3, lines 320140-320141, shows data relating to the source and location of the GAM oligonucleotide, specifically the GAM

PRECURSOR (hairpin) and its position in the genomic sequence of Herpes virus 5.

GAM NAME	PRECUR GAM ORGANISM	SOURCE	STR SRC-START	SRC-END
SEQ-ID		AND OFFSET	OFFSET	

sequence to the TARGET gene name as bound by the GAM RNA as set forth in SEQ ID NO: 117937. Table 6, lines 2093282 and 2093283 relate to target binding site SEQ ID NO: 2034243; lines 6630926 and 6630927 relate to target binding site SEQ ID NO: 3983175; lines 2093540 and 2093541 relate to target binding site SEQ ID NO: 2034310; lines 6638580 and 6638581 relate to target binding site SEQ ID NO: 3985198; line 6630929 relates to target binding site SEQ ID NO: 3983175; line 2093543 relates to target binding site SEQ ID NO: 2034310; line 6638583 relates to target binding site SEQ ID NO: 3985198; lines 2087866 and 2087867 relate to target binding site SEQ ID NO: 2032849; lines 663308 and 663309 relate to target binding site SEQ ID NO: 3983798; and line 2058344 relates to SEQ ID NO: 2024974.

TARGET BINDING SITE SEQ-ID	TARGET ORGANISM	TARGET	TARGET BINDING SITE SEQUENCE
2034243	Human herpesvirus 5	NC_001347 190696 - 19	GGGTGCACCTGCTGCCGCCACT
		3236 gene	
3983175	Human herpesvirus 5	NC_001347 190696 - 19	GGGTGCACCTGCTGCCGCCACT
		3236 gene	
2034310	Human herpesvirus 5	NC_001347 190696 - 19	GCTGATCGCGTCACT
		3236 gene	
3985198	Human herpesvirus 5	NC_001347 190696 - 19	GCTGATCGCGTCACT
		3236 gene	
3983175	Human herpesvirus 5	NP_040085.1 gene	GGGTGCACCTGCTGCCGCCACT
2034310	Human herpesvirus 5	NP_040085.1 gene	GCTGATCGCGTCACT
3985198	Human herpesvirus 5	NP_040085.1 gene	GCTGATCGCGTCACT

2032849 Human herpesvirus 5 NC_001347 54824 - 560 GTCGCCGTCAC
95 gene

3983798 Human herpesvirus 5 NC_001347 54824 - 560 GTCGCCGTCAC
95 gene

2024974 Human SFTPA1 TCCATCCTGAGGC

Table 7, lines 6493595-6493625 shows data relating to target-genes and binding sites of GAM oligonucleotides.

GAM NAME	GAM ORGANISM	GAM RNA	TARGET	TARGET	REF-ID	ORGANISM	TARGET; LOWER: GAM)	UTR BINDING SITE DRAW (UPPER: GAM	POS
=====									
GAM501831	Human herpesvirus 5	AGTGACGG	CGGTGCAC	NC_001347 1	Human herpes 3	-- G C C	GCTG C		A
	virus 5	AGGCTG	GCCACT	96 - 19 637			GT G C A GT-- A		
=====									
GAM501831	Human herpesvirus 5	AGTGACGG	CGGTGCAC	NP_0400 NC_001347 1	Human herpes 3	-- G C C	GCTG C		A
	virus 5	AGGCTG	GCCACT	96 - 19 637			GT G C A GT-- A		
=====									
GAM501831	Human herpesvirus 5	AGTGACGG	CGGTGCAC	NP_0400 NC_001347 1	Human herpes 3	-- G C C	GCTG C		A
	virus 5	AGGCTG	GCCACT	96 - 19 637			GT G C A GT-- A		
=====									
GAM501831	Human herpesvirus 5	AGTGACGG	CGGTGCAC	NP_0400 NC_001347 1	Human herpes 3	-- G C C	GCTG C		A
	virus 5	AGGCTG	GCCACT	96 - 19 637			GT G C A GT-- A		
=====									
GAM501831	Human herpesvirus 5	AGTGACGG	CGGTGCAC	NP_0400 NC_001347 1	Human herpes 3	-- G C C	GCTG C		A
	virus 5	AGGCTG	GCCACT	96 - 19 637			GT G C A GT-- A		
=====									
GAM501831	Human herpesvirus 5	AGTGACGG	CGGTGCAC	NP_0400 NC_001347 1	Human herpes 3	-- G C C	GCTG C		A
	virus 5	AGGCTG	GCCACT	96 - 19 637			GT G C A GT-- A		
=====									

GT G C AGT				
GAM501831	Human herpes AGTGACGG	GTCGCCGT NC_0013	NC_001347 5 Human herpes	3 -- - - - - - A
virus 5	TGAGATCC CACT	47 5482 4423 - 5482	virus 5	GTC G CCGTCACT
	AGGCTG	4 - 560.3		CGG C GGCAGTGA
	95 gene			
	GT A CTAGAGT			
GAM501831	Human herpes GCCITCCGG	TCCATCCT SFTPA1	NM_005411 Human	3 -- - - - - - T B
virus 5	ATCACATG GAGGC			T CCAT CC GAGGC
	GTTACT			A GGTA GG CTCCG
	TC TT CACTA C			

[213] It is appreciated that the specific functions and accordingly the utilities of each of a plurality of GAM oligonucleotides that are described by Fig. 1 are correlated with and may be deduced from the identity of the GAM TARGET GENES inhibited thereby, and whose functions are set forth in Table 8, hereby incorporated herein Table 8C, lines 4766438-4766618 shows data relating to the function and utilities of GAM RNA as set forth in SEQ ID NO: 117937.

GAM NAME	GAM RNA	GAM ORGANISM	TARGET	TARGET	GAM FUNCTION	GAM
SEQUENCE		ORGANISM				POS
=====	=====	=====	=====	=====	=====	=====
GAM501831	AGTGACGG	Human herpes NC_0013	Human her	GAM501831	is a viral miRNA-like oligonucleotide that is encode	A
	TGAGATCC	virus 5	47 1906 pesvirus	d by the Human herpesvirus 5 genome, which targets a viral tar		
	AGGCTG		96 - 19 5	get gene NC_001347 190696 - 193236 gene (UTR reference: NC_001		
			3236 ge	347 193237 - 193637) as part of an internal viral regulation m		
	ne		ne	echanism.		
				NC_001347 190696 - 193236 gene BINDING SITE 1 and NC_001347 19		
				0696 - 193236 gene BINDING SITE 2 are viral target binding sit		
				es that are found in the untranslated regions of mRNA encoded		
				by the NC_001347 190696 - 193236 gene gene, corresponding to t		
				arget binding sites such as BINDING SITE I, BINDING SITE II or		
				BINDING SITE III of Fig. 1. The nucleotide sequences of NC_00		
				1347 190696 - 193236 gene BINDING SITE 1 and NC_001347 190696		
				- 193236 gene BINDING SITE 2, and the complementary secondary		

structure to the nucleotide sequence of GAM501831 RNA are set forth in Tables 6-7, hereby incorporated herein.

A function of GAM501831 is to inhibit NC_001347 190696 - 193236 gene, a GAM501831 viral target gene which is associated with Human herpesvirus 5 infection, as part of an internal viral regulation mechanism. Accordingly, the utilities of GAM501831 include the diagnosis, prevention and treatment of Human herpesvirus 5 infection and associated clinical conditions.

GAM501831 AGTGACGG Human herpes NC_001347 190696 - 193236 gene BINDING SITE 1 and NC_001347 190696 - 193236 gene BINDING SITE 2 are viral target binding sites that are found in the untranslated regions of mRNA encoded by the NC_001347 190696 - 193236 gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of NC_001347 190696 - 193236 gene BINDING SITE 1 and NC_001347 190696 - 193236 gene BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM501831 RNA are set forth in Tables 6-7, hereby incorporated herein.

Another function of GAM501831 is to inhibit NC_001347 190696 - 193236 gene, a GAM501831 viral target gene which is associated with Human herpesvirus 5 infection, as part of an internal viral regulation mechanism. Accordingly, the utilities of GAM501831

GAM501831	AGTGACGG	Human herpes NP_0400	Human herpesvirus 5 genome, which targets a viral target
85.1	ge pesvirus	get gene NP_040085.1 gene (UTR reference: NC_001347 193237 - 193637)	as part of an internal viral regulation mechanism.
AGGCTG	ne	5	
			NP_040085.1 gene BINDING SITE 1 and NP_040085.1 gene BINDING SITE 2 are viral target binding sites that are found in the untranslated regions of mRNA encoded by the NP_040085.1 gene gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of NP_040085.1 gene BINDING SITE1 and NP_040085.1

gene BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM501831 RNA are set forth in

Tables 6-7, hereby incorporated herein.

Another function of GAM501831 is to inhibit NP_040085.1 gene, a GAM501831 viral target gene which is associated with Human herpesvirus 5 infection, as part of an internal viral regulation mechanism. Accordingly, the utilities of GAM501831 include the diagnosis, prevention and treatment of Human herpesvirus 5 infection and associated clinical conditions.

GAM501831 AGTACGCGG Human herpes NP_0400 Human herpesvirus 5 is a viral miRNA-like oligonucleotide that is encoded by

AGGCTG 5' TGAGATCC virus 5' 85.1 gene pesvirus d by the Human herpesvirus 5 genome, which targets a viral target

AGGCTG 5' TGAGATCC virus 5' 85.1 gene pesvirus d by the Human herpesvirus 5 genome, which targets a viral target (UTR reference: NC_001347 193237 - 193637) as part of an internal viral regulation mechanism.

NP_040085.1 gene BINDING SITE 1 and NP_040085.1 gene BINDING SITE 2 are viral target binding sites that are found in the untranslated regions of mRNA encoded by the NP_040085.1 gene

NP_040085.1 gene BINDING SITE 1 and NP_040085.1 gene BINDING SITE 2, corresponding to target binding sites such as BINDING SITE I

, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of NP_040085.1 gene BINDING SITE 1 and NP_040085.1

gene BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM501831 RNA are set forth in

Tables 6-7, hereby incorporated herein.

Another function of GAM501831 is to inhibit NP_040085.1 gene, a GAM501831 viral target gene which is associated with Human herpesvirus 5 infection, as part of an internal viral regulation mechanism. Accordingly, the utilities of GAM501831 include the diagnosis, prevention and treatment of Human herpesvirus 5

infection and associated clinical conditions.

Tables 6-7, hereby incorporated herein.

Another function of GAM501831 is to inhibit NP_040085.1 gene, a GAM501831 viral target gene which is associated with Human herpesvirus 5 infection, as part of an internal viral regulation mechanism. Accordingly, the utilities of GAM501831 include the diagnosis, prevention and treatment of Human herpesvirus 5

infection and associated clinical conditions.

Tables 6-7, hereby incorporated herein.

Another function of GAM501831 is to inhibit NP_040085.1 gene, a GAM501831 viral target gene which is associated with Human herpesvirus 5 infection, as part of an internal viral regulation mechanism. Accordingly, the utilities of GAM501831 include the diagnosis, prevention and treatment of Human herpesvirus 5

infection and associated clinical conditions.

Tables 6-7, hereby incorporated herein.

Another function of GAM501831 is to inhibit NP_040085.1 gene, a GAM501831 viral target gene which is associated with Human herpesvirus 5 infection, as part of an internal viral regulation mechanism. Accordingly, the utilities of GAM501831 include the diagnosis, prevention and treatment of Human herpesvirus 5

infection and associated clinical conditions.

infection and associated clinical conditions.

GAM501831 GCCTCCGG Human herpes SFTPAl Human GAM501831 is a viral miRNA-like oligonucleotide that is encode B
 ATCACAATG virus 5 d by the Human herpesvirus 5 genome, which targets a human hos
 GTTACT t gene Surfactant, pulmonary- associated protein A1 (SFTPAl, A
 ccession number: NM_005411) as part of a viral host-attacking
 mechanism.
 SFTPAl BINDING SITE is a human target binding site that is a f
 ound in the the 3' untranslated region of mRNA encoded by the
 SFTPAl gene, corresponding to a target binding site such as BI
 NDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. I
 he nucleotide sequences of SFTPAl BINDING SITE, and the comple
 mentary secondary structure to the nucleotide sequence of GAM5
 01831 RNA are set forth in Tables 6-7, hereby incorporated her
 ein.
 Another function of GAM501831 is to inhibit SFTPAl, a GAM50183
 1 human target gene which is involved in lipids and carbohydra
 tes metabolism. SFTPAl is associated with Human herpesvirus 5
 infection, and therefore GAM501831 is associated with the abo
 vementioned infection, as part of a novel viral mechanism of a
 ttacking a host. Accordingly, the utilities of GAM501831 inclu
 de the diagnosis, prevention and treatment of Human herpesviru
 s 5 infection and associated clinical conditions.
 The function of SFTPAl and its association with various diseas
 es and clinical conditions has been established by previous st
 udies, as described hereinabove with reference to GAM336913.

GAM501831 GCCTCCGG Human herpes SFTPAl Human GAM501831 is a viral miRNA-like oligonucleotide that is encode B

ATCACAIG virus 5	d by the Human herpesvirus 5 genome, which targets a human hos
GTTACT	t gene Surfactant, pulmonary- associated protein A1 (SFTPAl, A
	cession number: NM_005411) as part of a viral host-attacking
	mechanism.
	SFTPAl BINDING SITE is a human target binding site that is a f
	ound in the the 3' untranslated region of mRNA encoded by the
	SFTPAl gene, corresponding to a target binding site such as BI
	NDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. I
	he nucleotide sequences of SFTPAl BINDING SITE, and the comple
	mentary secondary structure to the nucleotide sequence of GAM5
	01831 RNA are set forth in Tables 6-7, hereby incorporated her
	ein.
	Another function of GAM501831 is to inhibit SFTPAl, a GAM50183
	1 human target gene which is involved in lipids and carbohydra
	tes metabolism. SFTPAl is associated with Human herpesvirus 5
	infection, and therefore GAM501831 is associated with the abo
	vementioned infection, as part of a novel viral mechanism of a
	ttacking a host. Accordingly, the utilities of GAM501831 inclu
	de the diagnosis, prevention and treatment of Human herpesviru
	s 5 infection and associated clinical conditions.
	The function of SFTPAl and its association with various diseases
	es and clinical conditions has been established by previous st
	udies, as described hereinabove with reference to GAM336913.

[214] Studies documenting the well known correlations between each of a plurality of GAM TARGET GENES that are described by Fig. 1 and the know gene functions and related discusses are listed in Table 9, hereby incorporated herein. Figure 9, lines 40832-40882, shows the GAM target genes and information related to the target gene.

SFTPAl	Human	Bruns, G.; Stroh, H.; Veldman, G. M.; Latt, S. A.; Floros, J.: The 35 kd
		pulmonary surfactant-associated protein is encoded on chromosome 10. Hum. Genet.

76: 58-62, 1987.

SFTPA1 Human Fisher, J. H.; Kao, F. T.; Jones, C.; White, R. T.; Benson, B. J.; Mason, R. J.:
The coding sequence for the 32,000-dalton pulmonary surfactant-associated
protein A is located on chromosome 10 and identifies two separate
restriction-fragment-length polymorphisms. Am. J. Hum. Genet. 40: 503-511, 1987.

SFTPA1 Human Floros, J.; DiAngelo, S.; Koptides, M.; Karinch, A. M.; Rogan, P. K.; Nielsen,
H.; Spragg, R. G.; Watterberg, K.; Deiter, G.: Human SP-A locus: allele
frequencies and linkage disequilibrium between the two surfactant protein A
genes. Am. J. Resp. Cell Molec. Biol. 15: 489-498, 1996.

SFTPA1 Human Floros, J.; Hoover, R. R.: Genetics of the hydrophilic surfactant proteins A and
D. Biochim. Biophys. Acta 1408: 312-322, 1998.

SFTPA1 Human Glasser, S. W.; Korfhagen, T. R.; Weaver, T.; Pilot-Matias, T.; Fox, J. L.;
Whitsett, J. A.: cDNA and deduced amino acid sequence of human pulmonary
surfactant-associated proteolipid SPL(Phe). Proc. Nat. Acad. Sci. 84: 4007-4011,
1987.

SFTPA1 Human Haataja, R.; Ramet, M.; Marttila, R.; Hallman, M.: Surfactant proteins A and B
as interactive genetic determinants of neonatal respiratory distress syndrome.
Hum. Molec. Genet. 9: 2751-2760, 2000.

SFTPA1 Human Kolble, K.; Lu, J.; Mole, S. E.; Kaluz, S.; Reid, K. B. M.: Assignment of the
human pulmonary surfactant protein D gene (SFTPD) to 10q22-q23 close to the
surfactant protein A gene cluster. Genomics 17: 294-298, 1993.

SFTPA1 Human Latt, S. A.: Personal Communication. Boston, Mass. 6/3/1987.

SFTPA1	Human	Moore, K. J.; D'Amore-Bruno, M. A.; Korfhagen, T. R.; Glasser, S. W.; Whitsett, J. A.; Jenkins, N. A.; Copeland, N. G.: Chromosomal localization of three pulmonary surfactant protein genes in the mouse. <i>Genomics</i> 12: 388-393, 1992.
SFTPA1	Human	Ramet, M.; Haataja, R.; Marttila, R.; Floros, J.; Hallman, M.: Association between the surfactant protein A (SP-A) gene locus and respiratory-distress syndrome in the Finnish population. <i>Am. J. Hum. Genet.</i> 66: 1569-1579, 2000.
SFTPA1	Human	Ramet, M.; Lofgren, J.; Albo, O.-P.; Hallman, M.: Surfactant protein-A gene locus associated with recurrent otitis media. <i>J. Pediatr.</i> 138: 266-268, 2001.
SFTPA1	Human	Selman, M.; Lin, H.-M.; Montano, M.; Jenkins, A. L.; Estrada, A.; Lin, Z.; Wang, G.; DiAngelo, S. L.; Guo, X.; Umstead, T. M.; Lang, C. M.; Pardo, A.; Phelps, D. S.; Floros, J.: Surfactant protein A and B genetic variants predispose to idiopathic pulmonary fibrosis. <i>Hum. Genet.</i> 113: 542-550, 2003.
SFTPA1	Human	White, R. T.; Damm, D.; Miller, J.; Spratt, K.; Schilling, J.; Hawgood, S.; Benson, B.; Cordell, B.: Isolation and characterization of the human pulmonary surfactant apoprotein gene. <i>Nature</i> 317: 361-363, 1985. --